1600 1635

OIPE

#7/ K.T. 1/25

Raw Seq Listing

ENTERED

RAW SEQUENCE LISTING DATE: 01/03/2002
PATENT APPLICATION: US/09/671,687A TIME: 14:55:14

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\01032002\I671687A.raw

<110> APPLICANT: WALLACH, David
KOVALENKO, Andrei
CANTARELLA, Giuseppina
<120> TITLE OF INVENTION: INHIBITOR OF NF-kB ACTIVATOR
<130> FILE REFERENCE: WALLACH=25
<140> CURRENT APPLICATION NUMBER: 09/671,687A
<141> CURRENT FILING DATE: 2000-09-28
<150> PRIOR APPLICATION NUMBER: 09/646,403
<151> PRIOR FILING DATE: 2000-09-18
<150> PRIOR APPLICATION NUMBER: IL 126024
<151> PRIOR FILING DATE: 1998-09-01
<150> PRIOR APPLICATION NUMBER: IL 134604
<151> PRIOR FILING DATE: 2000-02-17
<160> NUMBER OF SEQ ID NOS: 4
<170> SOFTWARE: PatentIn version 3.1
<210> SEQ ID NO: 1
<211> LENGTH: 2116
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (549)..(549)
<223> OTHER INFORMATION: n is either a, c, g, or t.
<220> FEATURE:
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<222> LOCATION: (562)..(562)
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<220> FEATURE:
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<222> LOCATION: (566)..(566)
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (652)..(652)
<223> OTHER INFORMATION: n is either a, c, g, or t.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (695)..(695)
<223> OTHER INFORMATION: n is either a, c, g, or t.
<400> SEQUENCE: 1

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cactgaccac cgagaacaga ttccactctt taccattcag tctcaccaag atgcccaata    120
ccaatggaag tattggccac agtccacttt ctctgtcagc ccagtctgta atggaagagc    180
taaacactgc acccgtccaa gagagtccac ccttggccat gcctcctggg aactcacatg    240
gtctagaagt gggctcattg gctgaagtta aggagaaccc tcctttctat ggggtaatcc    300
gttggatcgg tcagccacca ggactgaatg aagtgctcgc tggactggaa ctggaagatg    360
agtgtgcagg ctgtacggat ggaaccttca gaggcactcg gtatttcacc tgtgccctga    420
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     77 agaaggcgct gtttgtgaaa ctgaagagct gcaggcctga ctctaggttt gcatcattgc    480
     79 agccggtttc caatcaagat tgagcgctgt aactctttag catttggagg ctacttaagt    540
W--> 81 gaagtagtng aagaaaatac tnccanccaa aaatggaaaa agaargcttg gagataatga    600
W--> 83 ttggggaaag aagaaaggca tccaagggtc attacaattc ttgktactta gnactcaacc    660
W--> 85 ttattctkgc ttatttkgct tttagttctg ttctnggaca ctggtgttac tttagacccc    720
     87 aaagaaaaag aaacgatgtt agaatattwt wkwgmmaccc aagagctact gaggacagaa    780
     89 attgttaatc ctctgagaat atatggatat gtgtgtgcca caaaaattat gaaactgagg    840
     91 aaaatacttg aaaaggtgga ggctgcatca ggatttacct ctgaagaaaa agatcctgag    900
     93 gaattcttga atattctgtt tcatcatatt ttaagggtag aacctttgct aaaaataaga    960
     95 tcagcaggtc aaaaggtaca agattgttac ttctatcaaa tttttatgga aaaaaatgag   1020
     97 aaagttggcg ttcccacaat tcagcagttg ttagaatggt cttttatcaa cagtaacctg   1080
     99 aaatttgcag aggcaccatc atgtctgatt attcagatgc ctcgatttgg aaaagacttt   1140
    101 aaactattta aaaaattttt ccttctctgg aattagatat aacagattta cttgaagaca   1200
    103 ccccagacag tgccggatat gtggagggct tgcaatgtat gagtgtaaga atgctacgac   1260
    105 gatccggaca ccagctggaa aaacaagcag ttttgtaaaa cctgcaacac tcaagtccac   1320
    107 cttcatccga agaggctgaa tcataaatat aacccagtgt cacttcccaa agacttaccc   1380
    109 cgactgggag attggagaca cggctgcatc ccttgccaga atatggagtt atttgctgtt   1440
    111 ctctgcatag aaacaagcca ctatgttgct tttgtgaagt atgggaagga cgattctgcc   1500
    113 tggctcttct ttggacagca tggccgatcc gggatggtgg tcagaatggc tcaacattcc   1560
    115 cccaagtcmc ccmtgsccca gaagtaggag agtacttgga agatgtctcc tggaagaccc   1620
    117 tgsawtycct tggactccca ggagaatccc aaggctgtgc acgaagactg ctttgtgatg   1680
    119 ccatatatgt gccatgtacc cagagtccaa caatgagttt gtacaaataa ctgggggtca   1740
    121 tcgggaaagg caaagaaact ggaaggcaga gtccctaacg ttgcatctta ttcggagctg   1800
    123 gcagttctgt tcacggtcca ttgccggcaa tggatgtctt tgtggtgatg atccttcaga   1860
    125 aaaggatgcc tctgtttaaa aacaaattgc ttttgtgtcc ctgaagtatt taataagaag   1920
    127 cattttgcac tctagaaagt atgtttgtgt tggtttttta agaagtctaa atgaagttat   1980
    129 taatacctga agctttaagt taagtgcatt gatcatatga tatttttgga agcatacaat   2040
    131 tttaattgtc gaagtttaaa gcctctttta gtccattgag aatgtaaata aatgtgtctt   2100
    133 ctttatggaa aaaaaa                                                 2116
    136 <210> SEQ ID NO: 2
    137 <211> LENGTH: 3715
    138 <212> TYPE: DNA
    139 <213> ORGANISM: Homo sapiens
    141 <220> FEATURE:
    142 <221> NAME/KEY: misc_feature
    143 <222> LOCATION: (18)..(18)
    144 <223> OTHER INFORMATION: n is either a, c, g, or t.
    147 <220> FEATURE:
    148 <221> NAME/KEY: misc_feature
    149 <222> LOCATION: (22)..(22)
    150 <223> OTHER INFORMATION: n is either a, c, g, or t.
    153 <220> FEATURE:
    154 <221> NAME/KEY: misc_feature
    155 <222> LOCATION: (756)..(756)
    156 <223> OTHER INFORMATION: n is either a, c, g, or t.
    159 <220> FEATURE:
    160 <221> NAME/KEY: misc_feature
    161 <222> LOCATION: (1348)..(1348)
    162 <223> OTHER INFORMATION: n is either a, c, g, or t.
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Input Set : A:\sequence listing.txt
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165 <400> SEQUENCE: 2
166 ggggttttct tttacacntc tncggtaccg aactcggatc cactagtaac gggccgccag 60
168 tgtgctggaa attcggcacg agggtgtggg gagccggggc cggcccggga cgcgggctgg 120
170 ggagccgggg cgaggggcga cgccccgccg cccgagtttc ccccttttcta gggtgaggat 180
172 ggttctacac agccacccgg agttccttag ttgaaaggtg cgccctgctg tgacagaatg 240
174 tggtaattgt aatctttaac attttcatgt aaaacatatt tcctgatcat ctttccattg 300
176 tcttcatgga aaattgataa atatttgtgc cttccaactc tcgtcttggt tgaatgactt 360
178 catcttaata caacatggac accacgttgc tgaaaacatg ctttgggact gccactgaat 420
180 ttatcttttg cggttttatg acaaagttat tagtagtttc ccttttttga attagtattt 480
182 tgaagttaat atcacaatga gttcaggctt atggagccaa gaaaaagtca cttcacccta 540
184 ctgggaagag cggatttttt acttgcttct tcaagaatgc agcgttacag acaaacaaac 600
186 acaaaagctc cttaaagtac cgaagggaag tataggacag tatattcaag atcgttctgt 660
188 ggggcattca aggattcctt ctgcaaaagg caagaaaaat cagattggat taaaaattct 720
190 agagcaacct catgcagttc tctttgttga tgaaanggat gttgtagaga taaatgaaaa 780
192 gttcacagag ttacttttgg caattaccaa ttgtgaggag aggttcagcc tgtttaaaaa 840
194 cagaaacaga ctaagtaaag gcctccaaat agacgtgggc tgtcctgtga aagtacagct 900
196 gagatctggg gaagaaaaat ttcctggagt tgtacgcttc agaggacccc tgttagcaga 960
198 gaggacagtc tccggaatat tctttggagt tgaattgctg gaagaaggtc gtggtcaagg 1020
200 tttcactgac ggggtgtacc aagggaaaca gctttttcag tgtgatgaag attgtggcgt 1080
202 gtttgttgca ttggacaagc tagaactcat agaagatgat gacactgcat tggaaagtga 1140
204 ttacgcaggt cctggggaca caatgcaggt cgaacttcct cctttggaaa taaactccag 1200
206 agtttctttg aagggtggag aaacaataga atctggaaca gttatattct gtgatgtttt 1260
208 gccaggaaaa gaaagcttag gatatttgt tggtgtggac atggataacc ctattggcaa 1320
210 ctgggatgga agatttgatg gagtgcanct ttgtagtttt gcgtgtgttg aaagtacaat 1380
212 tctattgcac atcaatgata tcatcccaga gagtgtgacg caggaaagga ggcctcccaa 1440
214 acttgccttt atgtcaagag gtgttgggga caaaggttca tccagtcata ataaaccaaa 1500
216 ggctacagga tctacctcag accctggaaa tagaamcaga tctgaattat tttatacctt 1560
218 aaatgggtct tctgttgact cacaaccaca atccaaatca aaaaatacat ggtacattga 1620
220 tgaagttgca gaagaccctg caaaatctct tacagagata tctacagact ttgaccgttc 1680
222 ttcaccacca ctccagcctc ctcctgtgaa ctcactgacc accgagaaca gattccactc 1740
224 tttaccattc agtctcacca agatgcccaa taccaatgga agtattggcc acagtccact 1800
226 ttctctgtca gcccagtctg taatggaaga gctaaacact gcacccgtcc aagagagtcc 1860
228 acccttggcc atgcctcctg ggaactcaca tggtctagaa gtgggctcat tggctgaagt 1920
230 taaggagaac cctcctttct atggggtaat ccgttggatc ggtcagccac caggactgaa 1980
232 tgaagtgctc gctggactgg aactggaaga tgagtgtgca ggctgtacgg atggaacctt 2040
234 cagaggcact cggtatttca cctgtgccct gaagaaggcg ctgtttgtga aactgaagag 2100
236 ctgcaggcct gactctaggt ttgcatcatt gcagccggtt tccaatcaga ttgagcgctg 2160
238 taactcttta gcatttggag gctacttaag tgaagtagta gaagaaaata ctccaccaaa 2220
240 aatggaaaaa gaaggcttgg agataatgat tgggaagaag aaaggcatcc agggtcatta 2280
242 caattcttgt tacttagact caaccttatt ctgcttattt gcttttagtt ctgttctgga 2340
244 cactgtgtta cttagaccca aagaaaagaa cgatgtagaa tattatagtg aaacccaaga 2400
246 gctactgagg acagaaattg ttaatcctct gagaatatat ggatatgtgt gtgccacaaa 2460
248 aattatgaaa ctgaggaaaa tacttgaaaa ggtggaggct gcatcaggat ttacctctga 2520
250 agaaaaagat cctgaggaat tcttgaatat tctgtttcat catattttaa gggtagaacc 2580
252 tttgctaaaa ataagatcag caggtcaaaa ggtacaagat tgttacttct atcaaatttt 2640
254 tatggaaaaa aatgagaaag ttggcgttcc cacaattcag cagttgttag aatggtcttt 2700
256 tatcaacagt aacctgaaat ttgcagaggc accatcatgt ctgattattc agatgcctcg 2760
258 atttggaaaa gactttaaac tatttaaaaa aatttttcct tctctggaat taaatataac 2820
260 agatttactt gaagacactc ccagacagtg ccggatatgt ggagggcttg caatgtatga 2880

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262 gtgtagagaa tgctacgacg atccggacat ctcagctgga aaaatcaagc agttttgtaa   2940
264 aacctgcaac actcaagtcc accttcatcc gaagaggctg aatcataaat ataacccagt   3000
266 gtcacttccc aaagacttac ccgactggga ctggagacac ggctgcatcc cttgccagaa   3060
268 tatggagtta tttgctgttc tctgcataga aacaagccac tatgttgctt ttgtgaagta   3120
270 tgggaaggac gattctgcct ggctcttctt tgacagcatg gccgatcggg atggtggtca   3180
272 gaatggcttc aacattcctc aagtcacccc atgcccagaa gtaggagagt acttgaagat   3240
274 gtctctggaa gacctgcatt ccttggactc caggagaatc caaggctgtg cacgaagact   3300
276 gctttgtgat gcatatatgt gcatgtacca gagtccaaca atgagtttgt acaaataact   3360
278 ggggtcatcg ggaaaggcaa agaaactgaa ggcagagtcc taacgttgca tcttattcga   3420
280 gctggcagtt ctgttcacgt ccattgccgg caatggatgt ctttgtggtg atgatccttc   3480
282 agaaaaggat gcctctgttt aaaaacaaat tgcttttgtg tccctgaagt atttaataag   3540
284 aagcattttg cactctagaa agtatgtttg tgttggtttt ttaagaagtc taaatgaagt   3600
286 tattaatacc tgaagcttta agttaagtgc attgatcata tgatattttt ggaagcatac   3660
288 aattttaatt gtggaagttt aaagcctctt ttagtccatt gagaatgtaa ataaa        3715
291 <210> SEQ ID NO: 3
292 <211> LENGTH: 949
293 <212> TYPE: PRT
294 <213> ORGANISM: Homo sapiens
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299 1               5                  10                  15
302 Glu Glu Arg Ile Phe Tyr Leu Leu Leu Gln Glu Cys Ser Val Thr Asp
303             20                  25                  30
306 Lys Gln Thr Gln Lys Leu Leu Lys Val Pro Lys Gly Ser Ile Gly Gln
307         35                  40                  45
310 Tyr Ile Gln Asp Arg Ser Val Gly His Ser Arg Ile Pro Ser Ala Lys
311     50                  55                  60
314 Gly Lys Lys Asn Gln Ile Gly Leu Lys Ile Leu Glu Gln Pro His Ala
315 65                  70                  75                  80
318 Val Leu Phe Val Asp Glu Asp Val Val Glu Ile Asn Glu Lys Phe Thr
319                 85                  90                  95
322 Glu Leu Leu Leu Ala Ile Thr Asn Cys Glu Glu Arg Phe Ser Leu Phe
323             100                 105                 110
326 Lys Asn Arg Asn Arg Leu Ser Lys Gly Leu Gln Ile Asp Val Gly Cys
327         115                 120                 125
330 Pro Val Lys Val Gln Leu Arg Ser Gly Glu Glu Lys Phe Pro Gly Val
331     130                 135                 140
334 Val Arg Phe Arg Gly Pro Leu Leu Ala Glu Arg Thr Val Ser Gly Ile
335 145                 150                 155                 160
338 Phe Phe Gly Val Glu Leu Leu Glu Glu Gly Arg Gly Gln Gly Phe Thr
339                 165                 170                 175
342 Asp Gly Val Tyr Gln Gly Lys Gln Leu Phe Gln Cys Asp Glu Asp Cys
343             180                 185                 190
346 Gly Phe Val Ala Leu Asp Lys Leu Glu Leu Ile Glu Asp Asp Asp Thr
347         195                 200                 205
350 Ala Leu Glu Ser Asp Tyr Ala Gly Pro Gly Asp Thr Met Gln Val Glu
351     210                 215                 220
354 Leu Pro Pro Leu Glu Ile Asn Ser Arg Val Ser Leu Lys Gly Gly Glu
355 225                 230                 235                 240
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Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\01032002\I671687A.raw

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358 Thr Ile Glu Ser Gly Thr Val Ile Phe Cys Asp Val Leu Pro Gly Lys
359                 245                 250                 255
362 Glu Ser Leu Gly Tyr Phe Val Gly Val Asp Met Asp Asn Pro Ile Gly
363             260                 265                 270
366 Asn Trp Asp Gly Arg Phe Asp Gly Val Leu Cys Ser Phe Ala Cys Val
367         275                 280                 285
370 Glu Ser Thr Ile Leu Leu His Ile Asn Asp Ile Ile Pro Glu Ser Val
371     290                 295                 300
374 Thr Gln Glu Arg Arg Pro Pro Lys Leu Ala Phe Met Ser Arg Gly Val
375 305                 310                 315                 320
378 Gly Asp Lys Gly Ser Ser Ser His Asn Lys Pro Lys Ala Thr Gly Ser
379                 325                 330                 335
382 Thr Ser Asp Pro Gly Asn Arg Arg Ser Glu Leu Phe Tyr Thr Leu Asn
383             340                 345                 350
386 Gly Ser Ser Val Asp Ser Gln Pro Gln Ser Lys Ser Lys Asn Thr Trp
387         355                 360                 365
390 Tyr Ile Asp Glu Val Ala Glu Asp Pro Ala Lys Ser Leu Thr Glu Ile
391     370                 375                 380
394 Ser Thr Asp Phe Asp Arg Ser Ser Pro Pro Leu Gln Pro Pro Pro Val
395 385                 390                 395                 400
398 Asn Ser Leu Thr Thr Glu Asn Arg Phe His Ser Leu Pro Phe Ser Leu
399                 405                 410                 415
402 Thr Lys Met Pro Asn Thr Asn Gly Ser Ile Gly His Ser Pro Leu Ser
403             420                 425                 430
406 Leu Ser Ala Gln Ser Val Met Glu Glu Leu Asn Thr Ala Pro Val Gln
407         435                 440                 445
410 Glu Ser Pro Pro Leu Ala Met Pro Pro Gly Asn Ser His Gly Leu Glu
411     450                 455                 460
414 Val Gly Ser Leu Ala Glu Val Lys Glu Asn Pro Pro Phe Tyr Gly Val
415 465                 470                 475                 480
418 Ile Arg Trp Ile Gly Gln Pro Pro Gly Leu Asn Glu Val Leu Ala Gly
419                 485                 490                 495
422 Leu Glu Leu Glu Asp Glu Cys Ala Gly Cys Thr Asp Gly Thr Phe Arg
423             500                 505                 510
426 Gly Thr Arg Tyr Phe Thr Cys Ala Leu Lys Lys Ala Leu Phe Val Lys
427         515                 520                 525
430 Leu Lys Ser Cys Arg Pro Asp Ser Arg Phe Ala Ser Leu Gln Pro Val
431     530                 535                 540
434 Ser Asn Gln Ile Glu Arg Cys Asn Ser Leu Ala Phe Gly Gly Tyr Leu
435 545                 550                 555                 560
438 Ser Glu Val Val Glu Glu Asn Thr Pro Pro Lys Met Glu Lys Glu Gly
439                 565                 570                 575
442 Leu Glu Ile Met Ile Gly Lys Lys Lys Gly Ile Gln Gly His Tyr Asn
443             580                 585                 590
446 Ser Cys Tyr Leu Asp Ser Thr Leu Phe Cys Leu Phe Ala Phe Ser Ser
447         595                 600                 605
450 Val Leu Asp Thr Val Leu Leu Arg Pro Lys Glu Lys Asn Asp Val Glu
451     610                 615                 620
454 Tyr Tyr Ser Glu Thr Gln Glu Leu Leu Arg Thr Glu Ile Val Asn Pro
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Input Set : A:\sequence listing.txt
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L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2